REMARKS

Reconsideration of the present application is respectfully requested. Claims 1-61 are pending in the application. Claims 13-14, 16-32, 24-47 and 50-61 are withdrawn from consideration as being drawn to a non-elected invention. Claim 1 has been canceled and rewritten as claim 62. Support for 80% identity is found on page 6, line 11. Claims 1-3, 13-14, 28, 29, 41, and 42 have been canceled without prejudice. Applicant maintains the right to pursue these claims or aspects of these claims in continuing applications. New Claims 62-94 have been added. No new matter has been added.

Formal drawings will be submitted to replace the informal drawings.

The specification is objected to because page 39, line 19 and page 41, line 9 cite hyperlinks which are directed to Internet addresses which is not permitted under USPTO current policy. The specification has been amended to delete reference to the hyperlinks.

The specification is objected to because page 39, lines 6-7 and page 59, lines 13-14 recite sequences without sequence identifiers. The specification has been amended to recite sequence identifiers. A corrected CRF and paper copy of the Sequence Listing are submitted. No new matter is added.

Claims 15, 33, and 48-49 are objected to because they depend from non-elected inventions. Claim 15 has been amended to depend from new Claim 62. Claims 28 and 41, from which Claims 33 and 48-49 depend, have been canceled and rewritten as claim 93 and 94. The Examiner indicated that the claims of Group I and V are linked by claims 33 and 48-49. The Examiner further indicated that upon allowance of the linking claims, the restriction requirement as to the linked inventions shall be withdrawn.

Claims 1-12, 15, 33, and 48-49 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The Examiner states

that Claim 1, part (f) is indefinite for failing to recite the specific hybridization conditions which define the claimed high stringency.

The Examiner's attention is drawn to page 15, lines 9-11, where high stringency is defined. It is not required that the definition be included in the claims when the term is defined in the specification.

The Examiner objects to the reference to Vector nti in Claim 1, part (b). Claim 1 has been rewritten as new Claim 62 which does not include reference to Vector nti.

Claims 11-12 have been amended to add "transgenic" seed as suggested by the Examiner.

Claim 3 has been canceled without prejudice to expedite prosecution.

Claims 33 and 48-49 are objected to because they recite a "responsive" plant cell. Claims 28 and 41, from which Claims 33 and 48-49 depend, have been rewritten as claims 93 and 94 respectively and do not include "responsive".

Claims 1-12, 15, 33, and 48-49 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The Examiner objects to Claim 1, parts (b) and (d).

Claim 1 has been canceled and rewritten as Claim 62. In order to expedite prosecution, the subject matter of Claim 1, parts (b) and (d) is not included in new Claim 62. Claims 28 and 41, from which Claims 33 and 48-49 depend, have been rewritten as new claims 93 and 94 respectively in order to expedite prosecution.

The Examiner also rejects claims 33 and 48-49 because they encompass Lec1 polynucleotides from any source and it is unclear either from the specification or from the prior art whether the consensus sequence SEQ ID NO: 23 is common to all LEC1 polypeptides including those from non-plant sources.

Claims 28 and 41, from which Claims 33 and 48-49 depend, have been rewritten as new claims 93 and 94 respectively in order to expedite prosecution. The new claims require a LEC1 polynucleotide having specific requirements. New claim 88 contains the consensus SEQ ID NO: 23. The claim requires that the polynucleotide is from a plant other than *Arabidopsis*, as also required in original claim 1. The inventor was clearly in possession of the consensus sequence at the time of filing.

The Examiner further states that it is unclear if Applicants were in possession of any LEC1 polynucleotides at the time this application was filed.

The Examiner's assertion is respectfully traversed as numerous LEC1 polynucleotides are provided in the present application. In addition conserved regions and primers are disclosed (Figure 1, SEQ ID NO: 23 and original claims). Methods of isolating nucleic acids are described on page 13-17 and Examples 1-6 of the present application.

Claims 1-12 and 15 are rejected under 35 U.S.C. 101 and under 35 U.S.C. 112, first paragraph because the claimed invention is not supported by either a credible asserted utility or a well established utility.

The Examiner objects to 60% sequence identity, lack of recited function, and use of primers.

New claim 62 requires a nucleic acid capable of modulating the level of LEC1 protein. Thus, a function is recited. Evidence of utility is demonstrated by the examples in the present application. The *Arabidopsis* gene which has 49% identity to the claimed maize polynucleotide is disclosed in Lotan *et al.*, Cell, 93:1195-1205 (1998), A5 in the 1449 IDS submitted by Applicant. Claim 15 has been amended to depend from claim 62. New Claim 62 requires a percent identity (structure) and a function. Both can be readily determined by routine methods by those skilled in the art.

The Examiner further states that the specification is not enabling for a polynucleotide with 20-contiguous bases of SEQ ID NO:1 encoding a polypeptide having LEC1 activity.

Complementary (antisense) polynucleotides provide a valuable and useful means for down-regulation of a gene, page 5, line 33 to page 6, line 4 of the present application. New Claim 62 requires that the nucleic acid is capable of modulating the level of LEC1 protein. Therefore, the polynucleotides have a credible asserted utility. The use of antisense methodology is also a well-established utility.

Claims 1-12, 15, and 48-49 are rejected under 35 U.S.C. 102(e) as being anticipated by Harada *et al* US 6,235,975.

In particular the Examiner objects to Claim 1, parts (c) and (f). The Examiner cites the attached Sequence Search. The Sequence Search somehow compares amino acid and nucleotide sequences. Enclosed is a comparison of the nucleotides of SEQ ID NO:1 and Arabidopsis LEC1. There is 49% identity and no more than 15 contiguous nucleotides in common. Certainly the polynucleotides will not hybridize under highly stringent conditions.

As noted above Claim 1 has been rewritten as new Claim 62. Harada *et al* do not disclose or suggest the specific sequences recited in new Claim 62. Also Claim 15 has been amended to depend from claim 62. Claims 28 and 41, from which Claims 33 and 48-49 depend, have been rewritten as new Claims 93 and 94 respectively in order to expedite prosecution.

Claims 1-12 and 15 are rejected under 35 U.S.C. 102(b) as being anticipated by Boudet *et al* (US 5,451,514). The Examiner objects to claim 1, parts (i) and (f).

The hybridization conditions recited in part (d) of new Claim 62 are defined on page 15, lines 9-11. It is not required that the definition be included in the claims when the term is defined in the specification. "At least 25 nucleotides in length" is removed from new Claim 62 as not being necessary to the claim. The hybridization conditions determine the length of the homologous sequence necessary.

The polynucleotide in new Claim 62, part (f) is "fully" complementary. Boudet *et al* do not disclose or suggest the specific sequences recited in new Claim 62. Claim 15 has been amended to depend from Claim 62.

The Applicant confirms that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made.

Claims 1-12, 15, 33, 48-49 are rejected under 35 U.S.C. 103(a) as being unpatentable over Harada *et al* US 6,235,975 in view of Lotan *et al* (Cell, vol. 93, pp. 1195-1205.

New Claim 62 recites specific and non-obvious LEC1 sequences that are not disclosed or suggested in Harada *et al* or Lotan *et al* either separately or in combination. As noted above, Claim 15 has been amended to depend from claim 62. Also, Claims 28 and 41, from which Claims 33 and 48-49 depend, have been rewritten as new Claims 93 and 94 in order to expedite prosecution.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned **"Version with markings to show changes made."**

In view of the above amendments and comments, withdrawal of all of the rejections and allowance of the remaining claims is respectfully requested.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 6 of page 39 has been amended as follows:

4. A Sal-A20 oligo nucleotide: SEQ ID NO: 24, TCG ACC CAC GCG TCC GAA AAA AAA AAA AAA AAA AAA, removes clones containing a poly A tail but no cDNA.

Paragraph beginning at line 17 of page 39 has been amended as follows:

Gene identities were determined by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., *et al.,* (1993) J. Mol. Biol. 215:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches under default parameters for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm. The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. (1993) *Nature Genetics* 3:266-272) provided by the NCBI. In some cases, the sequencing data from two or more clones containing overlapping segments of DNA were used to construct contiguous DNA sequences.

Paragraph beginning at line 6 of page 41 has been amended as follows:

ESTs encoding plant transcription factors were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul, S. F., *et al.*, (1993) *J. Mol. Biol. 215*:403-410[; see also www.ncbi.nlm.nih.gov/BLAST/]) searches for similarity to sequences contained in the BLAST "nr" database (comprising all non-redundant GenBank CDS translations, sequences derived from the 3-dimensional structure Brookhaven Protein Data Bank, the last major release of the SWISS-PROT protein sequence database, EMBL, and DDBJ databases). The cDNA sequences obtained in Example 1 were analyzed for similarity to all publicly available DNA sequences contained in the "nr" database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the "nr" database using the BLASTX algorithm (Gish, W. and States, D. J. (1993) *Nature Genetics 3*:266-272 and Altschul, Stephen F., *et al.* (1997) *Nucleic Acids Res. 25*:3389-3402) provided by the NCBI.

Paragraph beginning at line 6 of page 59 has been amended as follows:

The presence of the maize LEC1 polynucleotide was analyzed by PCR using 100-200 ng template DNA in a 30 ml PCR reaction mixture containing 1X concentration enzyme buffer (10 mM Tris-HCl pH 8.8, 1.5 mM magnesium chloride, 50 mM potassium chloride, 0.1% Triton X-100), 200 µM dNTPs, 0.3 µM primers and 0.022 U TaqDNA polymerase (Boehringer Mannheim). Thermocycling conditions were as follows (30 cycles): denaturation at 95°C for 30 s, annealing at 55°C for 1 min and extension at 72°C for 1 min. Primer sequences (F=forward; R=reverse) used were: SEQ ID NO: 25, (F) 5'-CGC TCT GTC ACC TGT TGT ACT C-3', SEQ ID

NO: 26, (R) 5'-CGT GAT GAA GCT GAT GTA CTC C-3'. Approximate PCR product length was 620 bp.

In the Claims:

Claims 1-3, 13-14, 28, 29, 41, and 42 have been cancelled without prejudice.

Claims 4-5, 9, 11-12, 15, 30-33, 43-45, and 47-49 have been amended as follows:

4. (Amended) A vector comprising at least one nucleic acid of claim [1] 62.

5. (Amended) An expression cassette comprising at least one nucleic acid of claim [1] 62 operably linked to a promoter, wherein the nucleic acid is in sense or antisense orientation.

9. (Amended) A transgenic plant comprising [at least one expression cassette of claim 5] an isolated nucleic acid of claim 1.

11. (Amended) A transgenic seed from the transgenic plant of claim 9.

12. (Amended) The transgenic seed from the transgenic plant of claim 10.

15. (Amended) A ribonucleic acid sequence comprising a polynucleotide of claim 62 [encoding a protein of claim 13].

30. (Amended) The method of claim [30] 93 wherein the at least one polynucleotide is operably linked to a promoter driving expression in the plant cell.

31. (Amended) The method of claim [29] 93 further comprising growing the transformed embryo under plant growing conditions to produce a regenerated plant.

32. (Amended) The method of claim [29] 93 wherein the plant cell is from corn, soybean, sorghum, wheat, rice, alfalfa, sunflower, canola or cotton.

33. (Amended) A plant produced by the method of claim [29] 93.

43. (Amended) The method of claim [45] 94 wherein the at least one polynucleotide is operably linked to a promoter driving expression in a plant cell.

44. (Amended) The method of claim [42] 94 further comprising suppressing in the plant cell the expression of an FIE polycomb polynucleotide using sense or antisense methods.

45. (Amended) The method of claim [42] 94 further comprising growing the somatic embryo under plant growing conditions to produce a regenerated plant.

47. (Amended) The method of claim [43] 94 wherein the at least one polynucleotide is expressed in integument or nucellus tissue.

48. (Amended) A plant produced by the method of claim [42] 94.

49. (Amended) The plant of claim [49] 48, wherein the plant is male sterile.

New claims 62-94 have been added as follows:

62. An isolated nucleic acid capable of modulating the level of LEC1 protein, the isolated nucleic acid comprising a member selected from the group consisting of:

(a) a polynucleotide which encodes a polypeptide of SEQ ID NO: 2;

(b) a polynucleotide comprising at least 20 contiguous bases of SEQ ID NO: 1;

(c) a polynucleotide having at least 80% sequence identity to the entire sequence of SEQ ID NO: 1, wherein the % sequence identity is determined by GAP analysis using Gap Weight of 50 and Length Weight of 3;

(d) a polynucleotide which selectively hybridizes under high stringency conditions to the polynucleotide of SEQ ID NO: 1;

(e) a polynucleotide having the sequence set forth in SEQ ID NO: 1; and

(f) a polynucleotide fully complementary to a polynucleotide of (b) through (e).

63. An isolated nucleic acid capable of modulating the level of LEC1 protein, the isolated nucleic acid comprising a polynucleotide which encodes a polypeptide of SEQ ID NO: 2 or a polynucleotide fully complementary thereof.

64. An expression cassette comprising the isolated nucleic acid of claim 63.

65. A transgenic plant cell comprising the isolated nucleic acid of claim 63.

66. A transgenic plant comprising the isolated nucleic acid of claim 63.

67. A transgenic plant seed comprising the isolated nucleic acid of claim 63.

68. An isolated nucleic acid capable of modulating the level of LEC1 protein, the isolated nucleic acid comprising a polynucleotide comprising at least 20 contiguous bases of SEQ ID NO: 1 or a polynucleotide fully complementary thereof.

69. An expression cassette comprising the isolated nucleic acid of claim 68.

70. A transgenic plant cell comprising the isolated nucleic acid of claim 68.

71. A transgenic plant comprising the isolated nucleic acid of claim 68.

72. A transgenic plant seed comprising the isolated nucleic acid of claim 68.

73. An isolated nucleic acid capable of modulating the level of LEC1 protein, the isolated nucleic acid comprising a polynucleotide having at least 80% sequence identity to the entire sequence of SEQ ID NO: 1, wherein the % sequence identity is determined by GAP analysis using Gap Weight of 50 and Length Weight of 3 or a polynucleotide fully complementary thereof.

74. An expression cassette comprising the isolated nucleic acid of claim 73.

75. A transgenic plant cell comprising the isolated nucleic acid of claim 73.

76. A transgenic plant comprising the isolated nucleic acid of claim 73.

77. A transgenic plant seed comprising the isolated nucleic acid of claim 73.

78. An isolated nucleic acid capable of modulating the level of LEC1 protein, the isolated nucleic acid comprising a polynucleotide which selectively hybridizes under high stringency conditions to the polynucleotide of SEQ ID NO: 1 or a polynucleotide fully complementary thereof.

79. An expression cassette comprising the isolated nucleic acid of claim 78.

80. A transgenic plant cell comprising the isolated nucleic acid of claim 78.

81. A transgenic plant comprising the isolated nucleic acid of claim 78.

82. A transgenic plant seed comprising the isolated nucleic acid of claim 78.

83. An isolated nucleic acid capable of modulating the level of LEC1 protein, the isolated nucleic acid comprising a polynucleotide having the sequence set forth in SEQ ID NO: 1 or a polynucleotide fully complementary thereof.

84. An expression cassette comprising the isolated nucleic acid of claim 83.

85. A transgenic plant cell comprising the isolated nucleic acid of claim 83.

86. A transgenic plant comprising the isolated nucleic acid of claim 83.

87. A transgenic plant seed comprising the isolated nucleic acid of claim 83.

88. An isolated nucleic acid capable of modulating the level of LEC1 protein, the isolated nucleic acid comprising a polynucleotide encoding a polypeptide comprising the sequence set forth in SEQ ID NO: 23, wherein the polynucleotide is from a plant other than *Arabidopsis*.

89. An expression cassette comprising the isolated nucleic acid of claim 88.

90. A transgenic plant cell comprising the isolated nucleic acid of claim 88.

91. A transgenic plant comprising the isolated nucleic acid of claim 88.

92. A transgenic plant seed comprising the isolated nucleic acid of claim 88.

93. A method for inducing somatic embryogenesis in a plant cell, the method comprising introducing into the plant cell at least one LEC1 polynucleotide and growing the plant cell under conditions sufficient to stimulate the production of a somatic embryo, wherein the at least one LEC1 polynucleotide comprises a member selected from the group consisting of:

(a) a polynucleotide which encodes a polypeptide of SEQ ID NO: 2;

(b) a polynucleotide having at least 80% sequence identity to the entire sequence of SEQ ID NO: 1, wherein the % sequence identity is determined by GAP analysis using Gap Weight of 50 and Length Weight of 3;

(c) a polynucleotide which selectively hybridizes under high stringency conditions to the polynucleotide of SEQ ID NO: 1; and

(d) a polynucleotide having the sequence set forth in SEQ ID NO: 1.

94. A method for inducing apomixis in a cell of a plant seed, the method comprising introducing into the cell at least one LEC1 polynucleotide and growing the cell under conditions sufficient to stimulate the production of a somatic embryo, wherein the at least one LEC1 polynucleotide comprises a member selected from the group consisting of:

(a) a polynucleotide which encodes a polypeptide of SEQ ID NO: 2;

(b) a polynucleotide having at least 80% sequence identity to the entire sequence of SEQ ID NO: 1, wherein the % sequence identity is determined by GAP analysis using Gap Weight of 50 and Length Weight of 3;

(c) a polynucleotide which selectively hybridizes under high stringency conditions to the polynucleotide of SEQ ID NO: 1; and

(d) a polynucleotide having the sequence set forth in SEQ ID NO: 1.

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APPENDIX A

Gap DNA Sequence Alignment

Sequences compared (dna): CDPGP75R versus AtLec1

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GAP of: cgcdpgp75r.seq  check: 3304  from: 1  to: 837

   to: cgatlec1.seq  check: 3011  from: 1  to: 826

        Gap Weight:     50      Average Match: 10.000
     Length Weight:      3   Average Mismatch:  0.000

           Quality:   3637             Length:    852
             Ratio:  4.403               Gaps:      5
Percent Similarity: 48.705   Percent Identity: 48.705

      Match display thresholds for the alignment(s):
          | = IDENTITY;  : =   5;  . =   1

cgcdpgp75r.seq x cgatlec1.seq October 5, 1998 11:00  ..

                .         .         .         .         .
     1 ..............ATGGACTCCAGCAGCTTCCTCCCTGCCGCCGGCGC 35
                     | ||  || || |     |||     || || |
     1 GAATTGAACTTGGACCAGCACAGCAACAACCCAACCCCAATGACCAGCTC 50
                .         .         .         .         .
    36 GGAGAATGGCTCGGCGGCGGGCGGCGCCAACAATGGCGGCGCTGCTCAGC 85
        |  |  |   | |  || || | |   ||||||||   ||  |  ||||
    51 AGTCATAGTAGCCGGCGCCGGTGACAAGAACAATGGTATCGTGGTCCAGC 100
                .         .         .         .         .
    86 AGCATGCGGCGCCGGCGATCCGCGAGCAGGACCGGCTGATGCCGATCGCG 135
       ||||  |  |    | |   || ||||| ||||     |||||  |||||
   101 AGCAACCACCATGTGTGGCTCGTGAGCAAGACCAATACATGCCAATCGCA 150
                .         .         .         .         .
   136 AACGTGATCCGCATCATGCGGCGCGTGCTGCCGGCGCACGCCAAGATCTC 185
       |||||  ||  | ||||||||         | ||| | |||||||| |||||
   151 AACGTCATAAGAATCATGCGTAAAACCTTACCGTCTCACGCCAAAATCTC 200
                .         .         .         .         .
   186 GGACGACGCCAAGGAGACGATCCAGGAGTGCGTGTCGGAGTACATCAGCT 235
        |||||||||||  || |||||  || || || || || ||||||||||||
   201 TGACGACGCCAAAGAAACGATTCAAGAATGTGTCTCCGAGTACATCAGCT 250
                .         .         .         .         .
   236 TCATCACGGGGGAGGCCAACGAGCGGTGCCAGCGGGAGCAGCGCAAGACC 285
       ||  |  ||  ||  || ||||||||||| |||||  ||  |||||  ||  ||||||
   251 TCGTGACCGGTGAAGCCAACGAGCGTTGCCAACGTGAGCAACGTAAGACC 300
                .         .         .         .         .
   286 ATCACCGCCGAGGACGTGCTGTGGGCCATGAGCCGCCTCGGCTTCGACGA 335
       ||  ||  ||  ||  ||   |  ||  |||||  ||||||    ||  ||  |||||   |
   301 ATAACTGCTGAAGATATCCTTTGGGCTATGAGCAAGCTTGGGTTCGATAA 350
                .         .         .         .         .
   336 CTACGTCGAGCCGCTCGGCGCCTACCTCCACCGCTACCGCGAGTTCGAGG 385
       ||||||  ||  ||  |||   ||   |  |  |   ||||  |||||  |||  |  |||
   351 CTACGTGGACCCCCTCACCGTGTTCATTAACCGGTACCGTGAGATAGAGA 400
                .         .         .         .         .
   386 GCGACGCGCGCGGCGTCGGGCTCGTCCCGGGGGCCGCCCCATCGCGCGGC 435
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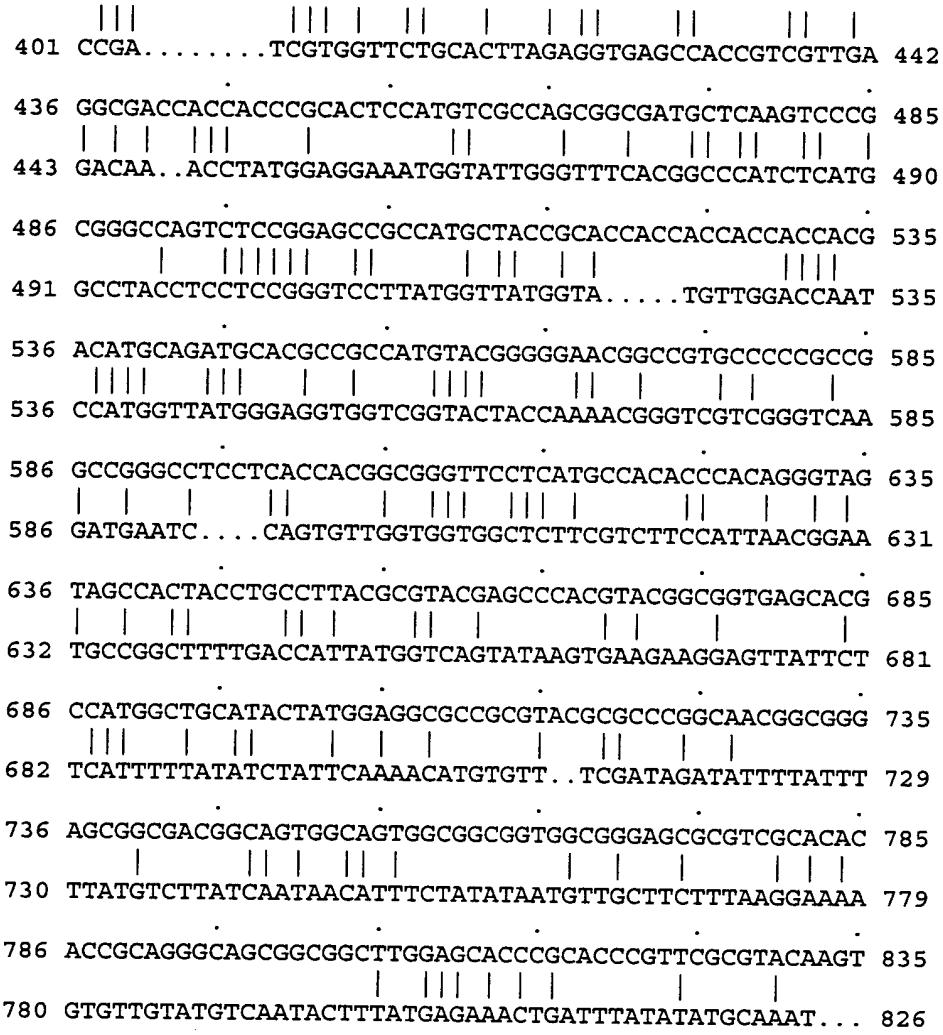

Conclusions: This Gap Nucleotide alignment between the Arabidopsis clone AtLec1 and the maize clone CDPGP75R compares most of their respective lengths, and reveals a 49% nucleotide identity.